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1600

RAW SEQUENCE LISTING   DATE: 02/12/2003
PATENT APPLICATION: **US/08/783,734D**   TIME: 11:15:26

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\02112003\H783734D.raw**

P.6

```
 3 <110> APPLICANT: Friedman, Jeffrey M.
 4        Lee, Gwo-Hua
 5        Proenca, Ricardo
 6        Ioffe, Ella
 8 <120> TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE
RECEPTOR, AND
 9        USES THEREOF
11 <130> FILE REFERENCE: 600-1-162CP2
13 <140> CURRENT APPLICATION NUMBER: US 08/783,734D
14 <141> CURRENT FILING DATE: 1997-01-16
16 <150> PRIOR APPLICATION NUMBER: US 08/599,974
17 <151> PRIOR FILING DATE: 1996-02-14
19 <150> PRIOR APPLICATION NUMBER: US 08/586,594
20 <151> PRIOR FILING DATE: 1996-01-16
22 <160> NUMBER OF SEQ ID NOS: 126
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 2529
28 <212> TYPE: DNA
29 <213> ORGANISM: Mus musculus
31 <400> SEQUENCE: 1
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34 ccatgccgga tcagcaccag cttgtagctc gtgccgaatt cggcacgagg ttgctttggg      120
36 aatgagcaag gtcaaaactg ctctgcactc acagacaaca ctgaagggaa gacactggct      180
38 tcagtagtga aggcttcagt ttttcgccag ctaggtgtaa actgggacat agagtgctgg      240
40 atgaaagggg acttgacatt attcatctgt catatggagc cattacctaa gaaccccttc      300
42 aagaattatg actctaaggt ccatctttta tatgatctgc ctgaagtcat agatgattcg      360
44 cctctgcccc cactgaaaga cagctttcag actgtccaat gcaactgcag tcttcgggga      420
46 tgtgaatgtc atgtgccggt acccagagcc aaactcaact acgctcttct gatgtatttg      480
48 gaaatcacat ctgccggtgt gagttttcag tcacctctga tgtcactgca gcccatgctt      540
50 gttgtgaaac ccgatccacc cttaggtttg catatggaag tcacagatga tggtaattta      600
52 aagatttctt gggacagcca acaatggca ccatttccgc ttcaatatca ggtgaaatat      660
54 ttagagaatt ctacaattgt aagagaggct gctgaaattg tctcagctac atctctgctg      720
56 gtagacagtg tgcttcctgg atcttcatat gaggtccagg tgaggagcaa gagactggat      780
58 ggttcaggag tctggagtga ctggagttca cctcaagtct ttaccacaca agatgttgtg      840
60 tattttccac ccaaaattct gactagtgtt ggatcgaatg cttcttttca ttgcatctac      900
62 aaaaacgaaa accagattat ctcctcaaaa cagatagttt ggtggaggaa tctagctgag      960
64 aaaatccctg agatacagta cagcattgtg agtgaccgag ttagcaaagt taccttctcc     1020
66 aacctgaaag ccaccagacc tcgagggaag tttacctatg acgcagtgta ctgctgcaat     1080
68 gagcaggcgt gccatcaccg ctatgctgaa ttatacgtga tcgatgtcaa tatcaatata     1140
70 tcatgtgaaa ctgacgggta cttaactaaa atgacttgca gatggtcacc cagcacaatc     1200
72 caatcactag tgggaagcac tgtgcagctg aggtatcaca ggcgcagcct gtattgtcct     1260
74 gatagtccat ctattcatcc tacgtctgag cccaaaaact gcgtcttaca gagagacggc     1320
76 ttttatgaat gtgttttcca gccaatcttt ctattatctg ctatacaat gtggatcagg     1380
```

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 78 atcaaccatt ctttaggttc acttgactcg ccaccaacgt gtgtccttcc tgactccgta   1440
 80 gtaaaaccac tacctccatc taacgtaaaa gcagagatta ctgtaaacac tggattattg   1500
 82 aaagtatctt gggaaaagcc agtctttccg gagaataacc ttcaattcca gattcgatat   1560
 84 ggcttaagtg gaaaagaaat acaatggaag acacatgagg tattcgatgc aaagtcaaag   1620
 86 tctgccagcc tgctggtgtc agacctctgt gcagtctatg tggtccaggt tcgctgccgg   1680
 88 cggttggatg gactaggata ttggagtaat tggagcagtc cagcctatac gcttgtcatg   1740
 90 gatgtaaaag ttcctatgag agggcctgaa ttttggagaa aaatggatgg ggacgttact   1800
 92 aaaaaggaga gaaatgtcac cttgctttgg aagcccctga cgaaaaatga ctcactgtgt   1860
 94 agtgtgagga ggtacgtggt gaagcatcgt actgcccaca tgggacgtgt gtcagaagat   1920
 96 gtgggaaatc ggaccaatct cactttcctg tggacagaac cagcgcacac tgttacagtt   1980
 98 ctggctgtca attccctcgg cgcttccctt gtgaatttta accttacctt ctcatggccc   2040
100 atgagtaaag tgagtgctgt ggagtcactc agtgcttatc ccctgagcag cagctgtgtc   2100
102 atcctttcct ggacactgtc acctgatgat tatagtctgt tatatctggt tattgaatgg   2160
104 aagatcctta atgaagatga tggaatgaag tggcttagaa ttccctcgaa tgttaaaaag   2220
106 ttttatatcc acgataattt tattcccatc gagaaatatc agtttagtct tacccagta    2280
108 tttatggaag gagttggaaa accaaagata attaatggtt tcaccaaaga tgctatcgac   2340
110 aagcagcaga tgacgcagg gctgtatgtc attgtaccca taattattc ctcttgtgtc     2400
112 ctactgctcg gaacactgtt aatttcacac cagagaatga aaaagttgtt ttgggacgat   2460
114 gttccaaacc ccaagaattg ttcctgggca caaggactga atttccaaaa gagaacggac   2520
116 actctttga                                                          2529
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119 <210> SEQ ID NO: 2
120 <211> LENGTH: 842
121 <212> TYPE: PRT
122 <213> ORGANISM: Mus musculus
124 <220> FEATURE:
125 <221> NAME/KEY: MISC_FEATURE
126 <222> LOCATION: (29)..(29)
127 <223> OTHER INFORMATION: X can be any amino acid
130 <400> SEQUENCE: 2
132 Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
133 1               5                   10                  15
136 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
137             20                  25                  30
140 Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
141             35                  40                  45
144 Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
145         50                  55                  60
148 Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
149 65                  70                  75                  80
152 Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
153                 85                  90                  95
156 Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
157             100                 105                 110
160 Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Leu Lys Asp Ser
161         115                 120                 125
164 Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
165         130                 135                 140
168 Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
169 145                 150                 155                 160
```

W--> appears at line 136 (marked in left margin).

```
172 Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
173             165             170             175
176 Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
177             180             185             190
180 Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
181             195             200             205
184 Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
185     210             215             220
188 Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
189 225             230             235             240
192 Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
193             245             250             255
196 Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
197             260             265             270
200 Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
201             275             280             285
204 Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
205     290             295             300
208 Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
209 305             310             315             320
212 Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
213             325             330             335
216 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
217             340             345             350
220 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
221     355             360             365
224 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
225     370             375             380
228 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
229 385             390             395             400
232 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
233             405             410             415
236 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
237             420             425             430
240 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
241     435             440             445
244 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
245     450             455             460
248 Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
249 465             470             475             480
252 Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
253             485             490             495
256 Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
257             500             505             510
260 Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
261             515             520             525
264 Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
265     530             535             540
268 Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
```

```
269 545                   550                   555                   560
272 Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
273             565                   570                   575
276 Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
277             580                   585                   590
280 Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
281         595                   600                   605
284 Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
285     610                   615                   620
288 Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
289 625                   630                   635                   640
292 Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
293             645                   650                   655
296 Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
297             660                   665                   670
300 Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
301         675                   680                   685
304 Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
305     690                   695                   700
308 Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
309 705                   710                   715                   720
312 Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
313             725                   730                   735
316 Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
317             740                   745                   750
320 Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
321         755                   760                   765
324 Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
325     770                   775                   780
328 Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
329 785                   790                   795                   800
332 Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
333             805                   810                   815
336 Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
337         820                   825                   830
340 Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
341         835                   840
344 <210> SEQ ID NO: 3
345 <211> LENGTH: 2848
346 <212> TYPE: DNA
347 <213> ORGANISM: Mus musculus
349 <220> FEATURE:
350 <221> NAME/KEY: misc_feature
351 <222> LOCATION: (44)..(44)
352 <223> OTHER INFORMATION: N can be A, C, T or G
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (67)..(67)
358 <223> OTHER INFORMATION: N can be A, C, T or G
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361 <220> FEATURE:
362 <221> NAME/KEY: misc_feature
363 <222> LOCATION: (234)..(234)
364 <223> OTHER INFORMATION: N can be A, C, T or G
367 <220> FEATURE:
368 <221> NAME/KEY: misc_feature
369 <222> LOCATION: (483)..(483)
370 <223> OTHER INFORMATION: N can be A, C, T or G
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (527)..(527)
376 <223> OTHER INFORMATION: N can be A, C, T or G
379 <220> FEATURE:
380 <221> NAME/KEY: misc_feature
381 <222> LOCATION: (564)..(564)
382 <223> OTHER INFORMATION: N can be A, C, T or G
385 <220> FEATURE:
386 <221> NAME/KEY: misc_feature
387 <222> LOCATION: (1237)..(1237)
388 <223> OTHER INFORMATION: N can be A, C, T or G
391 <220> FEATURE:
392 <221> NAME/KEY: misc_feature
393 <222> LOCATION: (1335)..(1335)
394 <223> OTHER INFORMATION: N can be A, C, T or G
397 <220> FEATURE:
398 <221> NAME/KEY: misc_feature
399 <222> LOCATION: (2038)..(2038)
400 <223> OTHER INFORMATION: N can be A, C, T or G
403 <220> FEATURE:
404 <221> NAME/KEY: misc_feature
405 <222> LOCATION: (2179)..(2179)
406 <223> OTHER INFORMATION: N can be A, C, T or G
409 <220> FEATURE:
410 <221> NAME/KEY: misc_feature
411 <222> LOCATION: (2182)..(2182)
412 <223> OTHER INFORMATION: N can be A, C, T or G
415 <220> FEATURE:
416 <221> NAME/KEY: misc_feature
417 <222> LOCATION: (2183)..(2183)
418 <223> OTHER INFORMATION: N can be A, C, T or G
421 <220> FEATURE:
422 <221> NAME/KEY: misc_feature
423 <222> LOCATION: (2219)..(2219)
424 <223> OTHER INFORMATION: N can be A, C, T or G
427 <220> FEATURE:
428 <221> NAME/KEY: misc_feature
429 <222> LOCATION: (2576)..(2576)
430 <223> OTHER INFORMATION: N can be A, C, T or G
433 <220> FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/12/2003
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:2; Xaa Pos. 29
Seq#:3; N Pos. 44,67,234,483,527,564,1237,1335,2038,2179,2182,2183,2219
Seq#:3; N Pos. 2576,2610
Seq#:4; Xaa Pos. 79
Seq#:5; N Pos. 160,258
Seq#:6; Xaa Pos. 14,19,25,58,67,68,84,86
Seq#:35; N Pos. 5
Seq#:39; N Pos. 55,62,72,143
Seq#:40; N Pos. 83,101,181
Seq#:41; N Pos. 193
Seq#:86; Xaa Pos. 29
Seq#:87; Xaa Pos. 29
Seq#:88; Xaa Pos. 29
Seq#:89; Xaa Pos. 79
Seq#:90; Xaa Pos. 14,19,25,58,67,68,84,86
Seq#:91; Xaa Pos. 79
Seq#:92; Xaa Pos. 14,19,25,58,67,68,84,86
```